



SEQUENCE LISTING

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Somerville, Chris S
Van de Loo, Frank

<120> PRODUCTION OF HYDROXYLATED FATTY ACIDS IN GENETICALLY MODIFIED PLANTS

<130> 56100-5005-01-US

<140> US 10/820,202

<141> 2004-04-08

<150> US 09/117,921

<151> 1999-03-04

<160> 15

<170> PatentIn version 3.2

<210> 1

<211> 543

<212> DNA

<213> Artificial sequence

<220>

<223> Nucleotide sequence of pLesq2

<220>

<221> misc_feature

<222> (83)..(83)

<223> n is a, c, g, or t

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ccacctaaaga aagctgcagt canatggtat gtcaaatacc tcaacaaccc tcttggacgc	120
attctggtgt taacagttca gtttatcctc ggggtggcctt tgtatctagc ctttaatgta	180
tcaggtagac cttatgatgg tttogettca catttcttcc ctcatgcacc tatctttaag	240
gaccgtgaac gtctccagat atacatctca gatgctggta ttctagctgt ctggttatgt	300
ctttaccgtt acgctgcttc acaaggattg actgctatga tctgcgtcta cggagtaccg	360
cttttgatag tgaacttttt ccttgtcttg gtcactttct tgcagcacac tcaccttca	420
ttacctcact atgattcaac cgagtgggaa tggattagag gagctttggt tacggtagac	480
agagactatg gaatcttgaa caaggtgttt cacaacataa cagacacca cgtagcacac	540
cac	543

<210> 2
 <211> 544
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleotide sequence of pLesq3

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 ccaaagcaga aatccgcaat caagtgggtac ggcgaatacc tcaacaaccc tcttggtcgc 120
 atcatgatgt taactgtcca gttcgctctc ggatggccct tgtacttagc cttcaacggt 180
 tctggcagac octacaatgg ttctgcttcc catttcttcc ccaatgctcc tatctacaac 240
 gaccgtgaac gctccagat ttacatctct gatgctggta ttctagccgt ctgttatggt 300
 ctttaccggt acgctgttgc acaaggacta gctcaatga tctgtctaaa cggagtcccg 360
 cttctgatag ttaacttttt cctcgtcttg atcacttact tacaacacac tcaccctgcg 420
 ttgctcact atgattcatc agagtgggat tggcttagag gagctttagc tactgtagac 480
 agagactatg gaatcttgaa caaggtgttc cataacatca cagacacca cgtcgcacac 540
 cact 544

<210> 3
 <211> 1855
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Nucleotide sequence of genomic clone encoding pLesq-HYD

<220>
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 <222> (46)..(46)
 <223> n is a, c, g, or t

<220>
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 <222> (99)..(99)
 <223> n is a, c, g, or t

<220>
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 <222> (203)..(203)
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<220>
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<222> (1658)..(1658)
 <223> n is a, c, g, or t

<220>
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 <222> (1788)..(1788)
 <223> n is a, c, g, or t

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 gacagttgaa gcaacaggaa caacaaggat ggttggtgnt gatgctgatg tggatgatgtg 120
 ttattcatca aataactaaat actacattac ttgttgctgc ctacttctcc tatttctctcc 180
 gccacccatt ttggaccac ganccttcca tttaaaccct ctctcgtgct attcaccaga 240
 agagaagcca agagagagag agagagaatg ttctgaggat cattgtcttc ttcatcgtaa 300
 ttaacgtaag ttttttttga ccaactcatat ctaaaatcta gtacatgcaa tagattaatg 360
 actgttctct cttttgatat ttctagcttc ttgaattcaa gatgggtgct ggtggaagaa 420
 taatggttac cccctcttcc aagaaatcag aaactgaagc cctaaaacgt ggaccatgtg 480
 agaaaccacc attcactggt aaagatctga agaaagcaat cccacagcat tgtttcaagc 540
 gotctatccc tcgttcttcc tctaccttc tcacagatat cactttagtt tcttgcttct 600
 actacgttgc cacaattac ttctctcttc ttctcagcc tctctctact tacctagctt 660
 ggctctctta ttgggtatgt caaggctgtg tcttaaccgg tatctgggtc attggccatg 720
 aatgtggtca ccatgcattc agtgactatc aatgggtaga tgacactgtt ggttttatct 780
 tccattcctt ccttctcgtc ccttacttct cctggaaata cagtcacgtc cgtcaccatt 840
 ccaacaatgg atctctcgag aaagatgaag tctttgtccc accgaagaaa gctgcagtca 900
 aatgggtatgt taaatacctc aacaaccctc ttggacgcac tctggtgtta acagttcagt 960
 ttatctctcg gtggcctttg tatctagcct ttaatgtatc aggtagacct tatgatggtt 1020
 togttcaca tttcttccct catgcacctc tctttaaaga ccgagaacgc ctccagatat 1080
 acatctcaga tgctggtatt ctagctgtct gttatggtct ttaccgttac gctgcttcac 1140
 aaggattgac tgctatgatc tgcgtctatg gagtaccgct tttgatagtg aactttttcc 1200
 ttgtcttggt aactttcttg cagcacactc atccttcgtt acctcattat gattcaaccg 1260
 agtgggaatg gattagagga gctttggtta cggtagacag agactatgga atattgaaca 1320
 aggtgttcca taacataaca gacacacatg tggctcatca tctctttgca actataaccg 1380
 attataacgc aatggaagct acagaggoga taaagccaat acttggtgat tactaccaact 1440

tcgatggaac accgtggtat gtggccatgt atagggaagc aaaggagtgt ctctatgtag 1500
 aaccggatac ggaacgtggg aagaaaggtg tctactatta caacaataag ttatgaggct 1560
 gatagggcga gagaagtgca attatcaatc ttcatttcca tgttttaggt gtcttgttta 1620
 agaagctatg ctttgtttca atastctcag agtccatnta gttgtgttct ggtgcatttt 1680
 gcctagttat gtgggtgctgg aagttagtgt tcaaactgct tctgtctgtg ctgcccagtg 1740
 aagaacaagt ttacgtgttt aaaatactcg gaacgaattg accacaanat atccaaaacc 1800
 ggctatccga attccatatc cgaaaaccgg atatccaaat ttccagagta cttag 1855

<210> 4
 <211> 384
 <212> PRT
 <213> *Lesquerella fendleri*

<400> 4

Met Gly Ala Gly Gly Arg Ile Met Val Thr Pro Ser Ser Lys Lys Ser
1 5 10 15

Glu Thr Glu Ala Leu Lys Arg Gly Pro Cys Glu Lys Pro Pro Phe Thr
20 25 30

Val Lys Asp Leu Lys Lys Ala Ile Pro Gln His Cys Phe Lys Arg Ser
35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Leu Thr Asp Ile Thr Leu Val Ser
50 55 60

Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
65 70 75 80

Leu Ser Thr Tyr Leu Ala Trp Pro Leu Tyr Trp Val Cys Gln Gly Cys
85 90 95

Val Leu Thr Gly Ile Trp Val Ile Gly His Glu Cys Gly His His Ala
100 105 110

Phe Ser Asp Tyr Gln Trp Val Asp Asp Thr Val Gly Phe Ile Phe His
115 120 125

Ser Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg
130 135 140

His His Ser Asn Asn Gly Ser Leu Glu Lys Asp Glu Val Phe Val Pro
 145 150 155 160

Pro Lys Lys Ala Ala Val Lys Trp Tyr Val Lys Tyr Leu Asn Asn Pro
 165 170 175

Leu Gly Arg Ile Leu Val Leu Thr Val Gln Phe Ile Leu Gly Trp Pro
 180 185 190

Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala
 195 200 205

Ser His Phe Phe Pro His Ala Pro Ile Phe Lys Asp Arg Glu Arg Leu
 210 215 220

Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
 225 230 235 240

Tyr Arg Tyr Ala Ala Ser Gln Gly Leu Thr Ala Met Ile Cys Val Tyr
 245 250 255

Gly Val Pro Leu Leu Ile Val Asn Phe Phe Leu Val Leu Val Thr Phe
 260 265 270

Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Thr Glu Trp
 275 280 285

Glu Trp Ile Arg Gly Ala Leu Val Thr Val Asp Arg Asp Tyr Gly Ile
 290 295 300

Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
 305 310 315 320

Leu Phe Ala Thr Ile Pro His Tyr Asn Ala Met Glu Ala Thr Glu Ala
 325 330 335

Ile Lys Pro Ile Leu Gly Asp Tyr Tyr His Phe Asp Gly Thr Pro Trp
 340 345 350

Tyr Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Leu Tyr Val Glu Pro
 355 360 365

Asp Thr Glu Arg Gly Lys Lys Gly Val Tyr Tyr Tyr Asn Asn Lys Leu
 370 375 380

<210> 5
 <211> 387
 <212> PRT
 <213> Ricinus communis

<400> 5

Met Gly Gly Gly Gly Arg Met Ser Thr Val Ile Thr Ser Asn Asn Ser
 1 5 10 15

Glu Lys Lys Gly Gly Ser Ser His Leu Lys Arg Ala Pro His Thr Lys
 20 25 30

Pro Pro Phe Thr Leu Gly Asp Leu Lys Arg Ala Ile Pro Pro His Cys
 35 40 45

Phe Glu Arg Ser Phe Val Arg Ser Phe Ser Tyr Val Ala Tyr Asp Val
 50 55 60

Cys Leu Ser Phe Leu Phe Tyr Ser Ile Ala Thr Asn Phe Phe Pro Tyr
 65 70 75 80

Ile Ser Ser Pro Leu Ser Tyr Val Ala Trp Leu Val Tyr Trp Leu Phe
 85 90 95

Gln Gly Cys Ile Leu Thr Gly Leu Trp Val Ile Gly His Glu Cys Gly
 100 105 110

His His Ala Phe Ser Glu Tyr Gln Leu Ala Asp Asp Ile Val Gly Leu
 115 120 125

Ile Val His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser
 130 135 140

His Arg Arg His His Ser Asn Ile Gly Ser Leu Glu Arg Asp Glu Val
 145 150 155 160

Phe Val Pro Lys Ser Lys Ser Lys Ile Ser Trp Tyr Ser Lys Tyr Ser
 165 170 175

Asn Asn Pro Pro Gly Arg Val Leu Thr Leu Ala Ala Thr Leu Leu Leu
 180 185 190

Gly Trp Pro Leu Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
195 200 205

Arg Phe Ala Cys His Tyr Asp Pro Tyr Gly Pro Ile Phe Ser Glu Arg
210 215 220

Glu Arg Leu Gln Ile Tyr Ile Ala Asp Leu Gly Ile Phe Ala Thr Thr
225 230 235 240

Phe Val Leu Tyr Gln Ala Thr Met Ala Lys Gly Leu Ala Trp Val Met
245 250 255

Arg Ile Tyr Gly Val Pro Leu Leu Ile Val Asn Cys Phe Leu Val Met
260 265 270

Ile Thr Tyr Leu Gln His Thr His Pro Ala Ile Pro Arg Tyr Gly Ser
275 280 285

Ser Glu Trp Asp Trp Leu Arg Gly Ala Met Val Thr Val Asp Arg Asp
290 295 300

Tyr Gly Val Leu Asn Lys Val Phe His Asn Ile Ala Asp Thr His Val
305 310 315 320

Ala His His Leu Phe Ala Thr Val Pro His Tyr His Ala Met Glu Ala
325 330 335

Thr Lys Ala Ile Lys Pro Ile Met Gly Glu Tyr Tyr Arg Tyr Asp Gly
340 345 350

Thr Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Lys Glu Cys Leu Phe
355 360 365

Val Glu Pro Asp Glu Gly Ala Pro Thr Gln Gly Val Phe Trp Tyr Arg
370 375 380

Asn Lys Tyr
385

<210> 6
<211> 383
<212> PRT

<213> Arabidopsis thaliana

<400> 6

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Glu Thr Asp Thr Thr Lys Arg Val Pro Cys Glu Lys Pro Pro Phe Ser
20 25 30

Val Gly Asp Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
35 40 45

Ile Pro Arg Ser Phe Ser Tyr Leu Ile Ser Asp Ile Ile Ile Ala Ser
50 55 60

Cys Phe Tyr Tyr Val Ala Thr Asn Tyr Phe Ser Leu Leu Pro Gln Pro
65 70 75 80

Leu Ser Tyr Leu Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
85 90 95

Leu Thr Gly Ile Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
100 105 110

Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
115 120 125

Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His
130 135 140

His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
145 150 155 160

Gln Lys Ser Ala Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
165 170 175

Gly Arg Ile Met Met Leu Thr Val Gln Phe Val Leu Gly Trp Pro Leu
180 185 190

Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Phe Ala Cys
195 200 205

His Phe Phe Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln

210	215	220
Ile Tyr Leu Ser Asp Ala Gly Ile Leu Ala Val Cys Phe Gly Leu Tyr		
225	230	235 240
Arg Tyr Ala Ala Ala Gln Gly Met Ala Ser Met Ile Cys Leu Tyr Gly		
	245	250 255
Val Pro Leu Leu Ile Val Asn Ala Phe Leu Val Leu Ile Thr Tyr Leu		
	260	265 270
Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp		
	275	280 285
Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu		
	290	295 300
Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu		
305	310	315 320
Phe Ser Thr Met Pro His Tyr Asn Ala Met Glu Ala Thr Lys Ala Ile		
	325	330 335
Lys Pro Ile Leu Gly Asp Tyr Tyr Gln Phe Asp Gly Thr Pro Trp Tyr		
	340	345 350
Val Ala Met Tyr Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp		
	355	360 365
Arg Glu Gly Asp Lys Lys Gly Val Tyr Trp Tyr Asn Asn Lys Leu		
	370	375 380

<210> 7
 <211> 384
 <212> PRT
 <213> Brassica napus

<220>
 <221> misc_feature
 <222> (384)..(384)
 <223> Xaa can be any naturally occurring amino acid
 <400> 7

Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser

1	5	10	15
Glu Thr Asp Asn Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr	20	25	30
Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser	35	40	45
Ile Pro Arg Ser Phe Ser His Leu Ile Trp Asp Ile Ile Ile Ala Ser	50	55	60
Cys Phe Tyr Tyr Val Ala Thr Thr Tyr Phe Pro Leu Leu Pro Asn Pro	65	70	75
Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val	85	90	95
Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His Ala Ala Phe	100	105	110
Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser	115	120	125
Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Arg His	130	135	140
His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Arg	145	150	155
Arg Ser Gln Thr Ser Ser Gly Thr Ala Ser Thr Ser Thr Thr Phe Gly	165	170	175
Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu Tyr	180	185	190
Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Ala Cys	195	200	205
His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu Gln	210	215	220
Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu Leu	225	230	235
			240

Pro Tyr Ala Ala Val Gln Gly Val Ala Ser Met Val Cys Phe Leu Arg
245 250 255

Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr Leu
260 265 270

Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp Asp
275 280 285

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
290 295 300

Asn Gln Gly Phe His Asn Ile Thr Asp Thr His Glu Ala His His Leu
305 310 315 320

Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala Ile
325 330 335

Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val Val
340 345 350

Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro Asp
355 360 365

Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu Xaa
370 375 380

<210> 8
<211> 309
<212> PRT
<213> Glycine max

<400> 8

Ser Leu Leu Thr Ser Phe Ser Tyr Val Val Tyr Asp Leu Ser Phe Ala
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Phe Ile Phe Tyr Ile Ala Thr Thr Tyr Phe His Leu Leu Pro Gln Pro
20 25 30

Phe Ser Leu Ile Ala Trp Pro Ile Tyr Trp Val Leu Gln Gly Cys Leu
35 40 45

Leu Thr Arg Val Cys Gly His His Ala Phe Ser Lys Tyr Gln Trp Val
50 55 60

Asp Asp Val Val Gly Leu Thr Leu His Ser Thr Leu Leu Val Pro Tyr
65 70 75 80

Phe Ser Trp Lys Ile Ser His Arg Arg His His Ser Asn Thr Gly Ser
85 90 95

Leu Asp Arg Asp Glu Arg Val Lys Val Ala Trp Phe Ser Lys Tyr Leu
100 105 110

Asn Asn Pro Leu Gly Arg Ala Val Ser Leu Leu Val Thr Leu Thr Ile
115 120 125

Gly Trp Pro Met Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp
130 135 140

Ser Phe Ala Ser His Tyr His Pro Tyr Arg Val Arg Leu Leu Ile Tyr
145 150 155 160

Val Ser Asp Val Ala Leu Phe Ser Val Thr Tyr Ser Leu Tyr Arg Val
165 170 175

Ala Thr Leu Lys Gly Leu Val Trp Leu Leu Cys Val Tyr Gly Val Pro
180 185 190

Leu Leu Ile Val Asn Gly Phe Leu Val Thr Ile Thr Tyr Leu Arg Val
195 200 205

His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Lys Gly Ala Leu Ala Thr
210 215 220

Met Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe His His Ile Thr
225 230 235 240

Asp Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His
245 250 255

Leu Arg Val Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Asp Thr
260 265 270

Pro Phe Tyr Lys Ala Leu Trp Arg Glu Ala Arg Glu Cys Leu Tyr Val

275		280		285
Glu Pro Asp Glu Gly Thr Ser Glu Lys Gly Val Tyr Trp Tyr Arg Asn				
290		295		300
Lys Tyr Leu Arg Val				
305				
<210> 9				
<211> 302				
<212> PRT				
<213> Glycine max				
<400> 9				
Phe Ser Tyr Val Val Tyr Asp Leu Thr Ile Ala Phe Cys Leu Tyr Tyr				
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Val Ala Thr His Tyr Phe His Leu Leu Pro Gly Pro Leu Ser Phe Arg				
	20		25	30
Gly Met Ala Ile Tyr Trp Ala Val Gln Gly Cys Ile Leu Thr Gly Val				
	35	40		45
Trp Val Val Ala Phe Ser Asp Tyr Gln Leu Leu Asp Asp Ile Val Gly				
	50	55	60	
Leu Ile Leu His Ser Ala Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr				
65		70	75	80
Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu				
	85		90	95
Val Phe Val Pro Lys Val Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg				
	100		105	110
Val Leu Thr Leu Ala Val Thr Leu Thr Leu Gly Trp Pro Leu Tyr Leu				
	115		120	125
Ala Leu Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr				
	130	135		140
Asp Pro Tyr Gly Pro Ile Tyr Ser Val Ile Ser Asp Ala Gly Val Leu				
145		150	155	160

Ala Val Val Tyr Gly Leu Phe Arg Leu Ala Met Ala Lys Gly Leu Ala
165 170 175

Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu Val Val Asn Gly Phe
180 185 190

Leu Val Leu Ile Thr Phe Leu Gln His Thr His Val Ser Glu Trp Asp
195 200 205

Trp Leu Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu
210 215 220

Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His Leu
225 230 235 240

Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Val Glu Tyr
245 250 255

Tyr Arg Phe Asp Glu Thr Pro Phe Val Lys Ala Met Trp Arg Glu Ala
260 265 270

Arg Glu Cys Ile Tyr Val Glu Pro Asp Gln Ser Thr Glu Ser Lys Gly
275 280 285

Val Phe Trp Tyr Asn Asn Lys Leu Ala Met Glu Ala Thr Val
290 295 300

<210> 10
<211> 372
<212> PRT
<213> Zea mays

<220>
<221> misc_feature
<222> (372)..(372)
<223> Xaa can be any naturally occurring amino acid

<400> 10

Met Gly Ala Gly Gly Arg Met Thr Glu Lys Glu Arg Glu Lys Gln Glu
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Gln Leu Ala Arg Ala Thr Gly Gly Ala Ala Met Gln Arg Ser Pro Val
20 25 30

Glu Lys Pro Pro Phe Thr Leu Gly Gln Ile Lys Lys Ala Ile Pro Pro
 35 40 45

His Cys Phe Glu Arg Ser Val Leu Lys Ser Phe Ser Tyr Val Val His
 50 55 60

Asp Leu Val Ile Ala Ala Ala Leu Leu Tyr Phe Ala Leu Ala Ile Ile
 65 70 75 80

Pro Ala Leu Pro Ser Pro Leu Arg Tyr Ala Ala Trp Pro Leu Tyr Trp
 85 90 95

Ile Ala Gln Gly Ala Phe Ser Asp Tyr Ser Leu Leu Asp Asp Val Val
 100 105 110

Gly Leu Val Leu His Ser Ser Leu Met Val Pro Tyr Phe Ser Trp Lys
 115 120 125

Tyr Ser His Arg Arg His His Ser Asn Thr Gly Ser Leu Glu Arg Asp
 130 135 140

Glu Val Phe Val Pro Lys Lys Lys Glu Ala Leu Pro Trp Tyr Thr Pro
 145 150 155 160

Tyr Val Tyr Asn Asn Pro Val Gly Arg Val Val His Ile Val Val Gln
 165 170 175

Leu Thr Leu Gly Trp Pro Leu Tyr Leu Ala Thr Asn Ala Ser Gly Arg
 180 185 190

Pro Tyr Pro Arg Phe Ala Cys His Phe Asp Pro Tyr Gly Pro Ile Tyr
 195 200 205

Asn Asp Arg Glu Arg Ala Gln Ile Phe Val Ser Asp Ala Gly Val Val
 210 215 220

Ala Val Ala Phe Gly Leu Tyr Lys Leu Ala Ala Ala Phe Gly Val Trp
 225 230 235 240

Trp Val Val Arg Val Tyr Ala Val Pro Leu Leu Ile Val Asn Ala Trp
 245 250 255

Leu Val Leu Ile Thr Tyr Leu Gln His Thr His Pro Ser Leu Pro His
 260 265 270

Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly Ala Leu Ala Thr Met
 275 280 285

Asp Arg Asp Tyr Gly Ile Leu Asn Arg Val Phe His Asn Ile Thr Asp
 290 295 300

Thr His Val Ala His His Leu Phe Ser Thr Met Pro His Tyr His Ala
 305 310 315 320

Met Glu Ala Thr Lys Ala Ile Arg Pro Ile Leu Gly Asp Tyr Tyr His
 325 330 335

Phe Asp Pro Thr Pro Val Ala Lys Ala Thr Trp Arg Glu Ala Gly Glu
 340 345 350

Cys Ile Tyr Val Glu Pro Glu Asp Arg Lys Gly Val Phe Trp Tyr Asn
 355 360 365

Lys Lys Phe Xaa
 370

<210> 11
 <211> 224
 <212> PRT
 <213> Ricinus communis

<400> 11

Trp Val Met Ala His Asp Cys Gly His His Ala Phe Ser Asp Tyr Gln
 1 5 10 15

Leu Leu Asp Asp Val Val Gly Leu Ile Leu His Ser Cys Leu Leu Val
 20 25 30

Pro Tyr Phe Ser Trp Lys His Ser His Arg Arg His His Ser Asn Thr
 35 40 45

Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys Lys Lys Ser Ser
 50 55 60

Ile Arg Trp Tyr Ser Lys Tyr Leu Asn Asn Pro Pro Gly Arg Ile Met
 65 70 75 80

Thr Ile Ala Val Thr Leu Ser Leu Gly Trp Pro Leu Tyr Leu Ala Phe
85 90 95

Asn Val Ser Gly Arg Pro Tyr Asp Arg Phe Ala Cys His Tyr Asp Pro
100 105 110

Tyr Gly Pro Ile Tyr Asn Asp Arg Glu Arg Ile Glu Ile Phe Ile Ser
115 120 125

Asp Ala Gly Val Leu Ala Val Thr Phe Gly Leu Tyr Gln Leu Ala Ile
130 135 140

Ala Lys Gly Leu Ala Trp Val Val Cys Val Tyr Gly Val Pro Leu Leu
145 150 155 160

Val Val Asn Ser Phe Leu Val Leu Ile Thr Phe Leu Gln His Thr His
165 170 175

Pro Ala Leu Pro His Tyr Asp Ser Ser Glu Trp Asp Trp Leu Arg Gly
180 185 190

Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile Leu Asn Lys Val Phe
195 200 205

His Asn Ile Thr Asp Thr Gln Val Ala His His Leu Phe Thr Met Pro
210 215 220

<210> 12
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 12
gctcttttgt gcgctcattc

20

<210> 13
<211> 20
<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<400> 13
cggtaccaga aaacgccttg

20

<210> 14
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<220>
<223> Primer

<220>
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<223> n is a, c, g, or t

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<223> n is a, c, g, or t

<400> 14
taywsncaym gnmgnca yca

20

<210> 15
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<212> DNA
<213> Artificial sequence

<220>
<223> Primer

<220>
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<222> (7)..(7)
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<220>
<221> misc_feature
<222> (10)..(10)
<223> n is a, c, g, or t

<220>
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<222> (16)..(16)
<223> n is a, c, g, or t

<400> 15
rtgrtgngcn acrtgngtrt c

21